

Exhibit 2: Alignment of Xenopus APC (Query) with Human APC (Subject)

> gb|AAA60353.1| **UG** polyposis locus-encoded protein
Length=2844

Score = 1360 bits (3520), Expect = 0.0, Method: Composition-based stats.
Identities = 747/861 (86%), Positives = 797/861 (92%), Gaps = 6/861 (0%)

| | | | |
|-------|-----|---|-----|
| Query | 1 | MAAASYDQLVKQVEALTMNTNLRQELEDNSNHLTKLETEATNMKEVLKQLQGSIEDEAM | 60 |
| | | MAAASYDQL+KQVEAL MEN+NLRQELEDNSNHLTKLETEA+NMKEVLKQLQGSIEDEAM | |
| Sbjct | 1 | MAAASYDQLLKQVEALKMENSNLRQELEDNSNHLTKLETEASNMEVLKQLQGSIEDEAM | 60 |
| Query | 61 | ASSGPIDLLERFKDLNLDSSNIPAGKARPKMSMRSYGSREGSLSGHSGECSPVPVGSFQR | 120 |
| | | ASSG IDLLER K+LNLDSSN P K R KMS+RSYGSREGS+S SGECSPPVP+GSF R | |
| Sbjct | 61 | ASSGQIDLLERLKLNLNLDSSNFPGVKLRKMSLSRSYGSREGSVSSRSGECSPPVPMGSFPR | 120 |
| Query | 121 | RGLLNGSRESAGYMEELEKERLLLLIAEHEKEEKEKRWYYAQLQNLTKRIDSLEPLTENFSM | 180 |
| | | RG +NGSRES GY+EELEKER LL+A+ +KEEKEK WYYAQLQNLTKRIDSLEPLTENFS+ | |
| Sbjct | 121 | RGFVNGSRESTGYLEELEKERSLLADLDKEEKEKDWYYAQLQNLTKRIDSLEPLTENFSL | 180 |
| Query | 181 | QTDMTRRQLEYEARQIRAAAMEEQLGTCQDMEKRVQTRVGKIHQIEEEILRIRQLLQSQVA | 240 |
| | | QTD+TRRQLEYEARQIR AMEEQLGTCQDMEKR Q R+ +I QIE++ILRIRQLLQSQ | |
| Sbjct | 181 | QTDLTTRRQLEYEARQIRVAMEEQLGTCQDMEKRAQRRIARIQQIEKDILRIRQLLQSQAT | 240 |
| Query | 241 | EAAERTPQSKHDAGSRDAEKLDPDQGTSEITASGNVSGQGSSSRADHDTTSMSSNSTY | 300 |
| | | EA ER+ Q+KH+ GS DAE+ +GQG EI + + G+GQGS++R DH+T SV+SS+ST+ | |
| Sbjct | 241 | EA-ERSSQNKHETGSHDAERQNEGQGVGEINMATS-GNGQGSTTRMDHETASVLSSSSTH | 298 |
| Query | 301 | SVPRRLTSHLGTKVEMVYSLLSMLGTHDKDDMSRTLLAMSSSQDSCIAMRQSGCLPLLIQ | 360 |
| | | S PRRLTSHLGTKVEMVYSLLSMLGTHDKDDMSRTLLAMSSSQDSCI+MRQSGCLPLLIQ | |
| Sbjct | 299 | SAPRRLTSHLGTKVEMVYSLLSMLGTHDKDDMSRTLLAMSSSQDSCISMRQSGCLPLLIQ | 358 |
| Query | 361 | LLHGNDKDSVLLGNSRGSKEARASGSAAALDNIHHSQPDDKGRGRREIRVLHLLLEQIRAYCE | 420 |
| | | LLHGNDKDSVLLGNSRGSKEARA SAAL NIIHSQPDDKGRGRREIRVLHLLLEQIRAYCE | |
| Sbjct | 359 | LLHGNDKDSVLLGNSRGSKEARARASAALHNIHHSQPDDKGRGRREIRVLHLLLEQIRAYCE | 418 |
| Query | 421 | TCWEWQEAHEQGMDQDKNPMPAPVDHQICPAVCVLMKLSFDEEHRHAMNELGGLQAI AEL | 480 |
| | | TCWEWQEAHE GMDQDKNPMPAPV+HQICPAVCVLMKLSFDEEHRHAMNELGGLQAI AEL | |
| Sbjct | 419 | TCWEWQEAHEPGMDQDKNPMPAPVEHQICPAVCVLMKLSFDEEHRHAMNELGGLQAI AEL | 478 |
| Query | 481 | LQVDCEMYGLINDHYSVTLRRYAGMALTNLTFGDVANKATLCMKSCMRALVAQLKSESE | 540 |
| | | LQVDCEMYGL NDHYS+TLRRYAGMALTNLTFGDVANKATLCMK CMRALVAQLKSESE | |
| Sbjct | 479 | LQVDCEMYGLTNDHYSITLRRYAGMALTNLTFGDVANKATLCMKGCMRALVAQLKSESE | 538 |
| Query | 541 | DLQQVIASVLRNLSWRADVNSKKTLEVGSVKALMECALDVKKESTLKSIVLSALWNLSAH | 600 |
| | | DLQQVIASVLRNLSWRADVNSKKTLEVGSVKALMECAL+VKKESTLKSIVLSALWNLSAH | |
| Sbjct | 539 | DLQQVIASVLRNLSWRADVNSKKTLEVGSVKALMECALEVKKESTLKSIVLSALWNLSAH | 598 |
| Query | 601 | CTENKADICSVDGALAFVLSTLTYSQTNTLAIIESGGGILRVSSLIATNEDHRQILRE | 660 |
| | | CTENKADIC+VDGALAFVL TLTYSQTNTLAIIESGGGILRVSSLIATNEDHRQILRE | |
| Sbjct | 599 | CTENKADICAVDGALAFVLGTLTYSQTNTLAIIESGGGILRVSSLIATNEDHRQILRE | 658 |

| | | | |
|-------|-----|--|-----|
| Query | 661 | NNCLQTLLQHLKSHSLTIVSNACGTLWNLSARNAKDQEGLDWMGAVSMLKNLIHSHKMI | 720 |
| | | NNCLQTLLQHLKSHSLTIVSNACGTLWNLSARN KDQE LDWMGAVSMLKNLIHSHKMI | |
| Sbjct | 659 | NNCLQTLLQHLKSHSLTIVSNACGTLWNLSARNPKDQEALWDMGAVSMLKNLIHSHKMI | 718 |
| Query | 721 | AMGSAAALRNLMANRPAKYKDANIMSPGSSVPSLHVRKQKALEAELDAQHLSETFDNIDN | 780 |
| | | AMGSAAALRNLMANRPAKYKDANIMSPGSS+PSLHVRKQKALEAELDAQHLSETFDNIDN | |
| Sbjct | 719 | AMGSAAALRNLMANRPAKYKDANIMSPGSSLPSLHVRKQKALEAELDAQHLSETFDNIDN | 778 |
| Query | 781 | LSPKTTHRNKQRHKQNLCSLEYALDSSRHDDSIKSDNFSIGNLTVLSPYINTTVLPSSSS | 840 |
| | | LSPK +HR+KQRHKQ+L +Y D++RHDD+ RSDNF+ GN+TVLSPY+NTTVLP SSS | |
| Sbjct | 779 | LSPKASHRSKQRHKQSLYGDYVFDTNRHDDN--RSDNFNTGNMTVLSPYLNTTVLPSSSS | 836 |
| Query | 841 | PRPTMDGSRPEKDR--ERTAG | 859 |
| | | R ++D SR EKDR ER G | |
| Sbjct | 837 | SRGSLDSSRSEKDRSLERER | 857 |

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